

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 13, 2003, 02:11:28 / Search time 129.415 seconds
(without alignments)
3373.191 Million cell updates/sec

Title: US-09-813-990a-1_copy_441_455

Perfect score: 15

Sequence: 1 ggttgcttctact 15

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vt.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vt.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rtd.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	45	100.0	2193	1	PIU44367
2	15	100.0	4902	3	AB048261
3	15	100.0	5263	1	FLRES
4	15	100.0	20916	1	AB006946
5	15	100.0	27330	1	M11237
6	15	100.0	85341	2	AC115342
7	15	100.0	101075	6	AC006430
8	15	100.0	103324	2	AC126433
9	15	100.0	138425	2	AC125755
10	15	100.0	153363	2	AC127395
11	15	100.0	165509	2	AC069886
12	15	100.0	167457	2	AC112446
13	15	100.0	157649	2	AC128090
14	15	100.0	158634	9	AL357472
15	15	100.0	172511	2	AC126462
16	15	100.0	172589	2	AC115562
17	15	100.0	176713	9	AP000751
18	15	100.0	176942	9	AC357520
19	15	100.0	188032	2	AC129339
20	15	100.0	189747	2	AC087291
21	15	100.0	190131	2	AC122368
22	15	100.0	192313	2	AF031265
23	15	100.0	195806	2	AC125580
24	15	100.0	213888	2	AC122506
25	15	100.0	221143	2	AC122263
26	15	100.0	231668	2	AC158881
27	15	100.0	241392	2	AC119239
28	15	100.0	245363	2	AL162453
29	14	93.3	780	6	AX414045
30	14	93.3	790	6	AX415217
31	14	93.3	841	9	BSA34151
32	14	93.3	896	6	AF105418
33	14	93.3	935	6	AF065379
34	14	93.3	1552	9	AF052392
35	14	93.3	1618	4	AF035435
36	14	93.3	1849	4	HSMAAP
37	14	93.3	2045	8	AY053138
38	14	93.3	2097	8	AY053134
39	14	93.3	3339	9	HUM50502
40	14	93.3	3772	9	HS056306
41	14	93.3	5495	10	M05380
42	14	93.3	6693	6	HC03835
43	14	93.3	8000	1	AF068902
44	14	93.3	8000	6	AX192753
45	14	93.3	10029	1	AF058439

ALIGNMENTS

RESULT 1
E044387
LOCUS
DEFINITION
Phizobium lequinosarum str. tritici 1071 qmef, complete cds. ORF2
gene, partial cds.
ACCESSION
044387
VERSION
044387.1
KEYWORDS
Phizobium lequinosarum str. tritici
Phizobium lequinosarum str. tritici
Bacterial Proteobacteria; alpha subdivision; Phizobiaceae group;
Phizobiaceae; Phizobium.
ORGANISM
Krol, J. and Skorupska, A.
REFERENCE
1 (bases 1 to 2193)
AUTHORS
TITLE
Identification of genes in Phizobium lequinosarum str. tritici

[illegible]

SR

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443. 4882
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443. 4883
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4455.4602
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100.0%; Score 15; DH 1; Length 5203;
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 derivative 0; Mismatches 0; Indels 0; Gaps 0;

CTGCT 15
|||
CTGCT 21:0

2056 bp DNA linear Eco 27-APR-2002
Mycobacterium tuberculosis H37Rv, section 72 of 280 of the
genome.

AE000518
1 611300583

Firmicutes: Actinobacteria: Actinobacteridae:
 Mycobacteriales: Mycobacteriaceae:
 Mycobacterium tuberculosis complex

genus; Mycobacterium tuberculosis complex.
1 to 29.6)

J., Percy, R., Dodson, R., Gehring, M., Hatt, C., Mackey, B.,
Lif, Nelson, W. G., Grayam, S. A., Ermolaeva, N.,
S. S., Deitcher, A., Ulmerback, T., Weidman, J., Kauri, E.,
M. K. L. A. and others.

Some Comparison of Mycobacterium tuberculosis Clinical and
v strains
ed

1 to 20915)
 on, R. D., Aland, O., Eisen, J. A., Carpenter, J., White, C.,
 J., DeKey, K., Zocsch, R., Winn, M., Hart, D., Hickey, E.

S. F., Nelson, W. C., Shiyah, L. A., Ermolaeva, M.,
S. L., Delcher, A., Utterback, I., Weidman, J., Khori, H.,
Mikula, A. and Bishai, W.
bacteria.

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Center Dr., Rockville, MD 20850, USA
Location/Qualifiers

1. 20916
/organism="Mycobacterium tuberculosis CDC1551"
/strain="CDC1551"

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/de_xref": "axon:83331"
/name": "clinical strain"
/element": 35.096

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sequence similarity; putative^a

BASE COUNT 11 a 17 c 9 g 14 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTGCTCCCG 11
DB 1 TTCTGCTCCCG 11

RESULT 6

AX122817/c AR122817 71 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 39 from patent US 6168778.
ACCESSION AR122817
VERSION AR122817.1 GI:14107783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 71)
Janjic,N., Gold,L., Schmidt,P. and Vargese,C.
TITLE Vascular endothelial growth factor (VEGF) Nucleic Acid Library
Complexes
JOURNAL Patent: US 6168778-A 39 02-JAN-2001;
FEATURES Location/Qualifiers
source 1..71
/organism="unknown"

BASE COUNT 19 a 18 c 26 g 8 t
ORIGIN

Query Match 100.0%; Score 11; DB 6; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTGCTCCCG 11
DB 23 TTCTGCTCCCG 13

RESULT 7

AX168155/c AX368155 144 bp DNA linear PAT 16-FEB-2002
LOCUS
DEFINITION Sequence 865 from Patent WO020454.4.
ACCESSION AX368155
VERSION AX368155.1 GI:18856228
KEYWORDS
SOURCE human.
ORGANISM human.

REFERENCE

1 Wang,T., Watanabe,Y., Henderson,R.A., Johnson,J.C., Retter,M.W.,
Marnerakis,M., Carter,D., Fanger,G.R., Vedvick,T.S., Bangui,C.S.,
McNabb,A., Fanger,N., Switzer,A., McNeill,P.D. and Clapper,J.G.
TITLE Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL Patent: WO 020454-A 865 17-JAN-2002;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..144
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT

23 a 50 c 37 g 34 t
ORIGIN

Query Match 100.0%; Score 11; DB 6; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTGCTCCCG 11

DB 132 TTCTGCTCCCG 128

RESULT 8

HS88A6F
LOCUS
DEFINITION H.sapiens CpG island DNA genomic MseI fragment, clone 88a6, forward
read cp988a6.r11a.
ACCESSION 263622
VERSION 263622.1 GI:103600
KEYWORDS CpG island; genomic MseI fragment.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.

REFERENCE

1 (bases 1 to 160)
Macdonald,M., Hocke,E., Wilkins,P. and Micklem,B.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
CB10 1HQ, England. E-mail contact: macquerry@sanger.ac.uk
REFERENCE 2 (bases 1 to 160)
CROSS,S.H., Charlton,J.A., Nau,X. and Bird,A.P.
TITLE Purification of CpG islands using a methylated DNA binding column.
JOURNAL Nat. Genet. 5 (3): 236-241 (1994)
MEDLINE 9428297.
PUBMED 512384

FEATURES

source
1..160
/organism="Homo sapiens"
/db_xref="taxon:9606"
/sex="male"
/issue_type="Epub"
/clone_lib="CGI-1"
/dev_stage="adult"
BASE COUNT 17 a 57 c 46 g 32 t 6 others
ORIGIN
Query Match 100.0%; Score 11; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTGCTCCCG 11
DB 89 TTCTGCTCCCG 99

RESULT 9

HS88A6R/c
LOCUS
DEFINITION H.sapiens CpG island DNA genomic MseI fragment, clone 88a6, reverse
read cp988a6.r11a.
ACCESSION 263623
VERSION 263623.1 GI:103600
KEYWORDS CpG island; genomic MseI fragment.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.

REFERENCE

1 (bases 1 to 160)
Macdonald,M., Hocke,E., Wilkins,P. and Micklem,B.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
CB10 1HQ, England. E-mail contact: macquerry@sanger.ac.uk
REFERENCE 2 (bases 1 to 160)
CROSS,S.H., Charlton,J.A., Nau,X. and Bird,A.P.
TITLE Purification of CpG islands using a methylated DNA binding column.

BASE COUNT

17 a 57 c 46 g 32 t 6 others
ORIGIN
Query Match 100.0%; Score 11; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTGCTCCCG 11
DB 89 TTCTGCTCCCG 99